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data("Tables")

Parameterize_vLiverPBPK <- function(MW,CLint,fub,pKa,Pow,
                                      species="Human",
                                      Davis.corrected=TRUE,
                                      model="well-stirred",BW=70)
{
  tissuelist <- list(Liver=c("Liver"),Kidney=c("Kidneys"),Lung=c("Lung"),Skin=c("Skin"),Gut=c("Gut"))

  if (!(species %in% colnames(PK.physiology.data)))
  {
    if (toupper(species) %in% toupper(colnames(PK.physiology.data)))
    {
      new.species <-
      colnames(PK.physiology.data)[toupper(colnames(PK.physiology.data))==toupper(species)]  

      warning(paste(species,"coerced to",new.species,"in Parameterize_vLiverPBPK"))
      species <- new.species
    } else stop (paste("Species",species,"not found in PK.physiology.data"))
  }
  out <-
  Predict_Ktissue2plasma(fub,pKa,Pow,tissuelist,species=species,Davis.corrected=Davis.corrected)
  CLmetabolism <-
  Calculate_Hepatic_Clearance(CLint,fub,out$flow[["Liver"]],out$vol[["Liver"]],model=model)
  return(list(
    BW = BW,
    Vartc = PK.physiology.data[PK.physiology.data$Parameter=="Plasma
Volume",species]/PK.physiology.data[PK.physiology.data$Parameter=="Hematocrit",species]/2/1000,
    Vvenc = PK.physiology.data[PK.physiology.data$Parameter=="Plasma
Volume",species]/PK.physiology.data[PK.physiology.data$Parameter=="Hematocrit",species]/2/1000,
    Vgutc = out$vol$Gut,
    Vliverc = out$vol$Liver,
    Vkidneyc = out$vol$Kidney,
    Vlungc = out$vol$Lung,
    Vdermc = out$vol$Skin,
    Vrestc = out$vol$Rest,
    Qcardiacc = PK.physiology.data[PK.physiology.data$Parameter=="Cardiac Output",species],
    Qgutf = out$flow$Gut/PK.physiology.data[PK.physiology.data$Parameter=="Cardiac Output",species],
    Qliverf = (out$flow$Liver-out$flow$Gut)/PK.physiology.data[PK.physiology.data$Parameter=="Cardiac
Output",species],
    Qkidneyf = out$flow$Kidney/PK.physiology.data[PK.physiology.data$Parameter=="Cardiac
Output",species],
    Qdermf = out$flow$Skin/PK.physiology.data[PK.physiology.data$Parameter=="Cardiac
Output",species],
    Qgfrc = PK.physiology.data[PK.physiology.data$Parameter=="GFR",species],
    hematocrit = PK.physiology.data[PK.physiology.data$Parameter=="Hematocrit",species],
    Krbc2plasma = out$Ktissue2plasma$"Red blood cells",
    Kliver2plasma = out$Ktissue2plasma$Liver,
    Kderm2plasma = out$Ktissue2plasma$Skin,
    Krest2plasma = out$Ktissue2plasma$Rest,
    Kkidney2plasma = out$Ktissue2plasma$Kidney,
    kgutabs = 1,
    kinhab = 1,
    kdermabs = 1,
    Fraction_unbound_plasma = fub,
    CLbiliary = 0,
  )
}

```

CLmetabolism = CLmetabolism

)  
}